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RAW SEQUENCE LISTING   DATE: 04/16/2002
PATENT APPLICATION: US/09/308,830A   TIME: 11:31:36

Input Set : A:\600-346SeqLst.txt
Output Set: N:\CRF3\04162002\I308830A.raw

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 3 <110> APPLICANT: Schlievert, Patrick M.
 4         Roggiani, Manuela
 5         Auge, Jennifer Stoehr
 6         Ohlendorf, Douglas
 8 <120> TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
10 <130> FILE REFERENCE: 600.346USWO
12 <140> CURRENT APPLICATION NUMBER: US 09/308,830A
13 <141> CURRENT FILING DATE: 1999-08-04
15 <150> PRIOR APPLICATION NUMBER: PCT/US97/22228
16 <151> PRIOR FILING DATE: 1997-12-05
18 <150> PRIOR APPLICATION NUMBER: US 60/032,930
19 <151> PRIOR FILING DATE: 1996-12-06
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Streptococcus sp.
30 <400> SEQUENCE: 1
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44 <211> LENGTH: 172
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53 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc          172
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57 <211> LENGTH: 172
58 <212> TYPE: DNA
59 <213> ORGANISM: Streptococcus sp.
61 <400> SEQUENCE: 4
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69 <210> SEQ ID NO: 5
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71 <212> TYPE: DNA
72 <213> ORGANISM: Streptococcus sp.
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79 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc           172
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 172
84 <212> TYPE: DNA
85 <213> ORGANISM: Streptococcus sp.
87 <400> SEQUENCE: 6
88 ccatcaccat caccaagaag aaataattac atattaaata caatacatat gtaataataa    60
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95 <210> SEQ ID NO: 7
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97 <212> TYPE: DNA
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100 <400> SEQUENCE: 7
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108 <210> SEQ ID NO: 8
109 <211> LENGTH: 172
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111 <213> ORGANISM: Streptococcus sp.
113 <400> SEQUENCE: 8
114 ccatcaccat caccaagaag aaataattac atattaaata caatacatat gtaataataa   60
116 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata  120
118 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc          172
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 172
123 <212> TYPE: DNA
124 <213> ORGANISM: Streptococcus sp.
126 <400> SEQUENCE: 9
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134 <210> SEQ ID NO: 10
135 <211> LENGTH: 172
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142 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata  120
144 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc          172
147 <210> SEQ ID NO: 11
148 <211> LENGTH: 31
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150 <213> ORGANISM: Streptococcus sp.
152 <400> SEQUENCE: 11
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158 <212> TYPE: DNA
159 <213> ORGANISM: Streptococcus sp.
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (828)..(1580)
164 <223> OTHER INFORMATION:
167 <400> SEQUENCE: 12
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170 tctatccttg aaacaggtgc aacatagatt agggcatgga gatttaccag acaactatga     120
172 acgtatatac tcacatcacg caatcggcaa ttgatgacat tggaactaaa ttcaatcaat     180
174 ttgttactaa caagcaacta gattgacaac taattctcaa caaacgttaa tttaacaaca     240
176 ttcaagtaac tcccaccagc tccatcaatg cttaccgtaa gtaatcataa cttactaaaa     300
178 ccttgttaca tcaaggtttt ttcttttgt cttgttcatg agttaccata actttctata     360
180 ttattgacaa ctaaattgac aactcttcaa ttatttttct gtctactcaa agtttcttc     420
182 atttgatata gtctaattcc accatcactt cttccactct ctctaccgtc acaacttcat     480
184 catctctcac ttttttcgtgt ggtaacacat aatcaaatat ctttccgttt ttacgcacta     540
186 tcgctactgt gtcacctaaa atataccccct tatcaatcgc ttctttaaac tcatctatat     600
188 ataacatatt tcatcctcct acctatctat tcgtaaaaag ataaaaataa ctattgtttt     660
190 ttttgttatt ttataataaa attattaata taagttaatg ttttttaaaa atatacaatt     720
192 ttattctatt tatagttagc tattttttca ttgttagtaa tattggtgaa ttgtaataac     780
194 ctttttaaat ctagaggaga acccagatat aaaatggagg aatatta atg gaa aac     836
195                                                       Met Glu Asn
196                                                         1
198 aat aaa aaa gta ttg aag aaa atg gta ttt ttt gtt tta gtg aca ttt     884
199 Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe
200     5                  10                  15
202 ctt gga cta aca atc tcg caa gag gta ttt gct caa caa gac ccc gat     932
203 Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp
204 20                  25                  30                  35
206 cca agc caa ctt cac aga tct agt tta gtt aaa aac ctt caa aat ata     980
207 Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile
208                 40                  45                  50
210 tat ttt ctt tat gag ggt gac cct gtt act cac gag aat gtg aaa tct    1028
211 Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser
212             55                  60                  65
214 gtt gat caa ctt tta tct cac cat tta ata tat aat gtt tca ggg cca    1076
215 Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro
216         70                  75                  80
218 aat tat gat aaa tta aaa act gaa ctt aag aac caa gag atg gca act    1124
219 Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr
220     85                  90                  95
222 tta ttt aag gat aaa aac gtt gat att tat ggt gta gaa tat tac cat    1172
223 Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His
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224 100                 105              110                 115
226 ctc tgt tat tta tgt gaa aat gca gaa agg agt gca tgt atc tac gga     1220
227 Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly
228             120                 125                 130
230 ggg gta aca aat cat gaa ggg aat cat tta gaa att cct aaa aag ata     1268
231 Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile
232             135                 140                 145
234 gtc gtt aaa gta tca atc gat ggt atc caa agc cta tca ttt gat att     1316
235 Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile
236         150                 155                 160
238 gaa aca aat aaa aaa atg gta act gct caa gaa tta gac tat aaa gtt     1364
239 Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val
240     165                 170                 175
242 aga aaa tat ctt aca gat aat aag caa cta tat act aat gga cct tct     1412
243 Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser
244 180                 185                 190                 195
246 aaa tat gaa act gga tat ata aag ttc ata cct aag aat aaa gaa agt     1460
247 Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser
248             200                 205                 210
250 ttt tgg ttt gat ttt ttc cct gaa cca gaa ttt act caa tct aaa tat     1508
251 Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr
252             215                 220                 225
254 ctt atg ata tat aaa gat aat gaa acg ctt gac tca aac aca agc caa     1556
255 Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln
256         230                 235                 240
258 att gaa gtc tac cta aca acc aag taacttttg cttttggcaa ccttacctac     1610
259 Ile Glu Val Tyr Leu Thr Thr Lys
260     245                 250
262 tgctggattt agaaatttta ttgcaattct tttattaatg taaaaaccgc tcatttgatg     1670
264 agcggttttg tcttatctaa aggagcttta cctcctaatg ctgcaaaatt ttaaatgttg     1730.
266 gattttgta tttgtctatt gtatttgatg ggtaatccca tttttcgaca gacatcgtcg     1790
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270 c                                                                    1851
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274 <211> LENGTH: 251
275 <212> TYPE: PRT
276 <213> ORGANISM: Streptococcus sp.
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285             20                  25              30
288 Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
289         35                  40              45
292 Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
293     50                  55              60
296 Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
297 65                  70              75                  80
300 Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
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301                     85                  90                  95
304 Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
305             100                 105                 110
308 Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
309         115                 120                 125
312 Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
313     130                 135                 140
316 Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
317 145                 150                 155                 160
320 Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
321             165                 170                 175
324 Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
325         180                 185                 190
328 Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
329         195                 200                 205
332 Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
333     210                 215                 220
336 Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
337 225                 230                 235                 240
340 Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
341             245                 250
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